

600-1-200

(Sheet 1 of 15)

CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT	48
Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr	
1 5 10 15	
AGA ATT TTG AGA CTC CAT GAA AAT GCA GAT TTT CAA GAC ACA ACT CTG	96
Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu	
20 25 30	
GAG AGT CAA GAT ACA AAA TTA ATA CCT GAT TCA TGT AGG AGA ATT AAA	144
Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys	
35 40 45	
CAG GCC TTT CAA GGA GCT GTG CAA AAG GAA TTA CAA CAT ATC GTT GGA	192
Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly	
50 55 60	
TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA	240
Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu	
65 70 75 80	
GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC	288
Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu	
85 90 95	
ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG	336
Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu	
100 105 110	
TCC TCT TGG TAC CAT GAT CCG GGG TGG GGT AAG ATC TCC AAC ATG ACT	384
Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr	
115 120 125	
TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAT TAC CTG	432
Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu	
130 135 140	
TAT GCC AAC ATT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT	480
Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala	
145 150 155 160	
ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA	528
Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys	
165 170 175	
ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC ACC AAG TAT TGG	576
Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp	
180 185 190	
TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC GTT GGT GGA TTT	624
Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe	
195 200 205	
TTT AAG TTA CCG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC	672
Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro	
210 215 220	
TCC TTA CTG GAT CCG GAT CAG GAT GCA ACA TAC TTT GGG GCT TTT AAA	720
Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys	
225 230 235 240	

Figure 1

GTT CGA GAT ATA GAT TGA GCCCCAGTTT TTGGAGTGT ATGTATTTC 768
 Val Arg Asp Ile Asp *
 245
 TGGATGTTTG GAAACATTTT TTAACAACAG CCAAGAAAGA TGTATATAGG TGTGTGAGAC 828
 TACTAAGAGG CATGGCCCAA CGGTACACGA CTCAGTATCC ATGCTCTTGA CCTGTAGAG 888
 AACACGCGTA TTTACAGCCA GTGGGAGATG TTAGACTCAT GGTGTGTTAC ACAATGGTTT 948
 TTAAATTTTG TAATGAATTC CTAGAATTAA ACCAGATTGG AGCAATTACG GGTGACCTT 1008
 ATGAGAACT GCATGTGGGC TATGGGAGGG GTTGGTCCCT GGTGATGTGC CCCTTCGCAG 1068
 CTGAAGTGA GAGGGTGCA TCTAGCGCAA TTGAAGGATC ATCTGAAGGG GCAAATTCCT 1128
 TTGAATGTG ACATCATGCT GGAACCTGCA AAAAATACTT TTTCTAATGA GGAGAGAAAA 1188
 TATATGTATT TTTATATAAT ATCTAAAGTT ATATTTCAGA TGTAAATGTT TCTTTGCAAA 1248
 GTATTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA ATATTAAAA ATGTCTTGCT 1308
 GTTGACATAT TTAATGTTTT AAATGTACAG ACATATTTAA CTGGTGCACT TTGTAAATTC 1368
 CCTGGGAAA ACTTGCAGCT AAGGAGGGA AAAAATGTTG TTTCTAATA TCAAATGCAG 1428
 TATATTTCTT CGTCTTTTT AAGTTAATAG ATTTTTCAG ACTTGTCAAG CCTGTGCAAA 1488
 AAAATTAAAA TGGATGCCTT GAATAATAAG CAGGATGTTG GCCACCAGGT GCCTTTCAAA 1548
 TTTAGAACT AATTGACTTT AGAAAGCTGA CATTGCCAAA AAGGATACAT AATGGGCCAC 1608
 TGAAATCTGT CAAGAGTAGT TATATAATTG TTGAACAGGT GTTTTTCCAC AAGTGCCGCA 1668
 AATTGTACCT TTTTTGTTT TTTTCAAAAT AGAAAAGTTA TTAGTGGTTT ATCAGCAAAA 1728
 AAGTCCAATT TTAATTTAGT AAATGTTATC TTATACTGTA CAATAAAAC ATTGCCTTTG 1788
 AATGTTAATT TTTTGGTACA AAAGTCGACG GCCGC 1823

Figure 1 (continued)

Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
 1 5 10 15
 Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
 20 25 30
 Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
 35 40 45
 Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
 50 55 60
 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
 65 70 75 80
 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
 85 90 95
 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
 100 105 110
 Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
 115 120 125
 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
 130 135 140
 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
 145 150 155 160
 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
 165 170 175
 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
 180 185 190
 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
 195 200 205
 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
 210 215 220
 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
 225 230 235 240
 Val Arg Asp Ile Asp *
 245

Figure 2

CCCACGTCCC GGGGAGCCAC TGCCAGGACC TTTGTGAACC GGTCCGGGCG GGGGCCGTGG	60
CGGAGTCTGC TCGGCGGTGG GTGGCCCAG AAGGGAGAGA ACGATCGCGG AGCAGGGCGC	120
CCGAAC'TCCG GCGGCCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys	171
250 255	
TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His	219
260 265 270	
GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro	267
275 280 285	
CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu	315
290 295 300	
GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln	363
305 310 315 320	
ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg	411
325 330 335	
ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu	459
340 345 350	
AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe	507
355 360 365	
CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg	555
370 375 380	
TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala	603
385 390 395 400	
CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn	651
405 410 415	
GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp	699
420 425 430	
TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn	747
435 440 445	
GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn	795
450 455 460	
ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr	843
465 470 475 480	

Figure 3

CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser 485 490 495	891
TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn 500 505 510	939
TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu 515 520 525	987
CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu 530 535 540	1035
GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp 545 550 555 560	1083
ATA GAC TGA GACTCATTTC GTGGAACATT AGCATGGATG TCCTAGATGT Ile Asp *	1132
TTGGAAACTT CTTAAAAAAT GGATGATGTC TATACATGTG TAAGACTACT AAGAGACATG	1192
GCCCCACGGTG TATGAACTC ACAGCCCTCT CTCCTGAGCC CTGTACAGGT TGTGTATATG	1252
TAAAGTCCAT AGGTGATGTT AGATTCATGG TGATTACACA ACGGTTTTAC AATTTTGTA	1312
TGATTTCTTA GAATTGAACC AGATTGGGAG AGGTATTCCG ATGCTTATGA AAAACTTACA	1372
CGTGAGCTAT GGAAGGGGGT CACAGTCTCT GGTCTAACCC CTGGACATGT GCCACTGAGA	1432
ACCTTGAAAT TAAGAGGATG CCATGTCATT GCATAGAAAT GATAGTGTGA AGGGTTAAGT	1492
TCTTTTGAAT TGTACATTG CGCTGGGACC TGCAAATAAG TTCTTTTTTCTAATGAGGA	1552
GAAAAATATA TGTATTTTTTA TATAATGTCT AAAGTTATAT TTCAGGTGTA ATGTTTTCTG	1612
TGCAAAGTTT TGTAAATTAT ATTGTGCTA TAGTATTTGA TTCAAATAT TTAAAAATGT	1672
CTCACTGTTG ACATATTTAA TGTTTTAAAT GTACAGATGT ATTTAACTGG TGCACTTTGT	1732
AATTCCTCTG AAGGTACTCG TAGCTAAGGG GGCAGAATAC TGTTCTGGT GACCACATGT	1792
AGTTTATTTT TTTATTTCTT TTAACCTAAT AGAGTCTTCA GACTTGTCAG AACTATGCAA	1852
GCAAAATAAA TAAATAAAAA TAAAATGAAT ACCTTGAATA ATAAGTAGGA TGTGGTCAC	1912
CAGGTGCCTT TCAAAATTTAG AAGCTAATTG ACTTTAGGAG CTGACATAGC CAAAAAGGAA	1972
CATAATAGGC TACTGAAATC TGTCAGGAGT ATTTATGCAA TTATTGAACA GGTGCTTTTT	2032
TTTACAAGAG CTACAAATTG TAAATTTTGG TTTCTTTTTT TTCCCATAGA AAATGTACTA	2092
TAGTTTATCA GCCAAAAAAC AATCCACTTT TTAATTTAGT GAAAGTTATT TTATTATACT	2152
GTACAATAAA AGCATGTGCT CTGAATGTTA ATTTTTTGGT AAAAAAATA AATTTGTACG	2212
AAAAAAAAA AAAAAAAAAA AAAAA	2237

Figure 3 (continued)

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Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
 1 5 10 15
 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
 20 25 30
 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser
 35 40 45
 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60
 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75 80
 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
 85 90 95
 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
 100 105 110
 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
 115 120 125
 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
 130 135 140
 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
 145 150 155 160
 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
 165 170 175
 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
 180 185 190
 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
 195 200 205
 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
 210 215 220
 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
 225 230 235 240
 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
 245 250 255
 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
 260 265 270
 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
 275 280 285
 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
 290 295 300
 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp *
 305 310 315

Figure 4

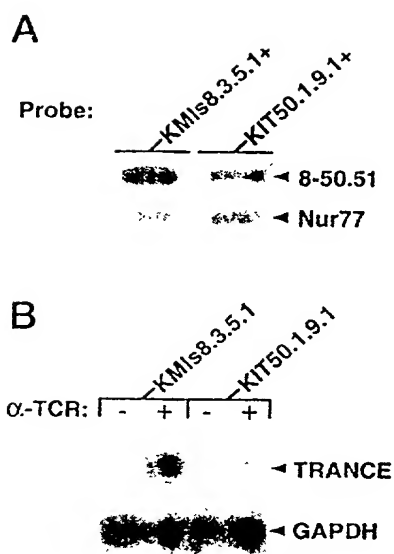


Figure 5

A

1 MRRASRDYCEYLKSSFLMRGAGVPVPHGHGLHPLACAPAPAPPPAAAGRSMFLALLGLGLGO mTRACE

61 VVCSLALFLYFAQMDPNRISEDSHICFYRILRIIEHAGLQDSTLESEUT--LPDSCFRM mTRACE
.....G...J.....DF..T...O..KL...I hTRACE

119 KQAFQAVQKELOHIVGQRFSGADAMMEGGWLDVAORGKPEAQFFAHITINAASTPSGS mTRACE
.....S.HTRAER..VD.....L.K.S.L.....TD..... hTRACE

179 HKVTILSGWYIHDPGWAKIS*IMTISNGKLRLVNQGFYYLYANICFRHHIETGGSVPTDYLOLM mTRACE
.....S.....G.....F.....DIA.E..... hTRACE

239 VYVVKTKLIPSSHINI.MKLSSTKNWSSGNSSEFIHYSINVGGFFKLRAGEKLSIQVSNPSLL mTRACE
...T.....T.....Y.....S.....E..... hTRACE

299 DPMQDATYRCAPFVQDID 316 mTRACE
.....R..... hTRACE

B

[illegible]

Figure 6

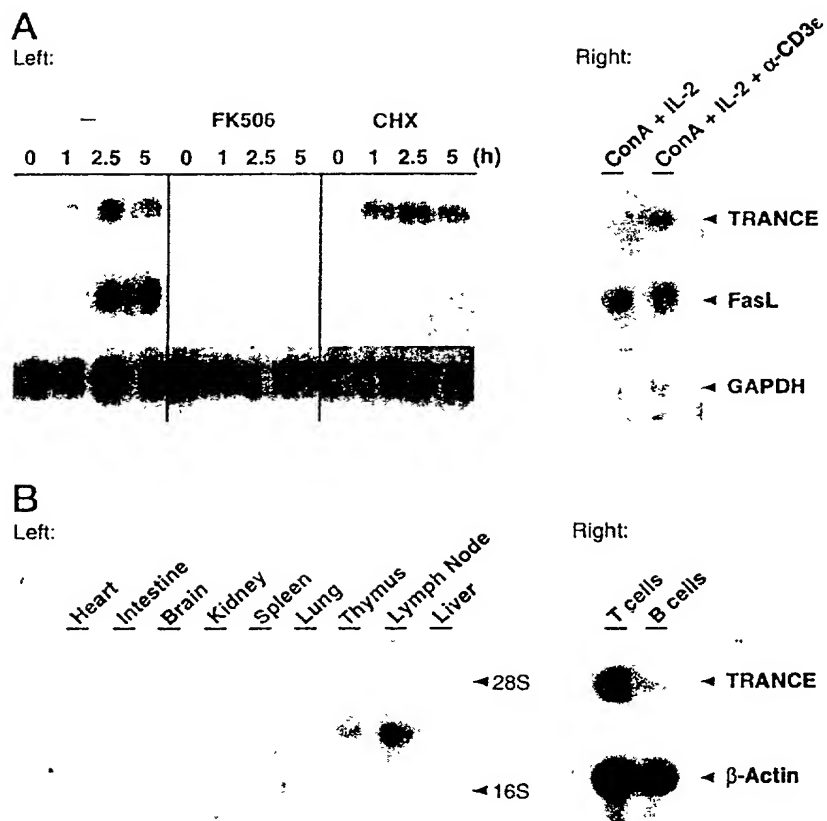


Figure 7

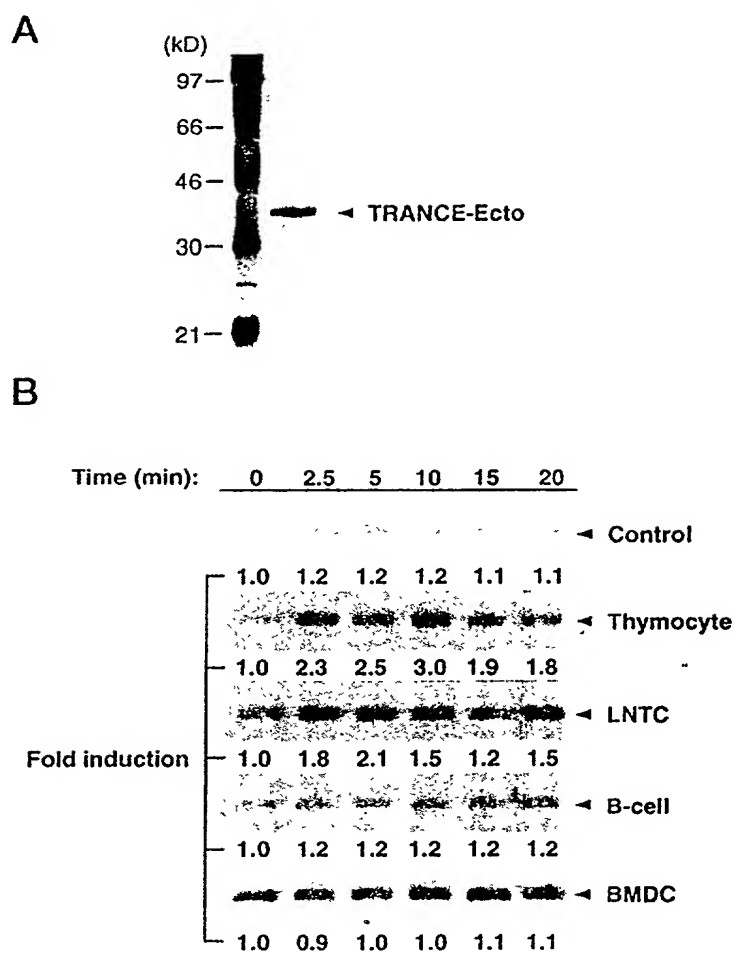


Figure 8

600-1-200

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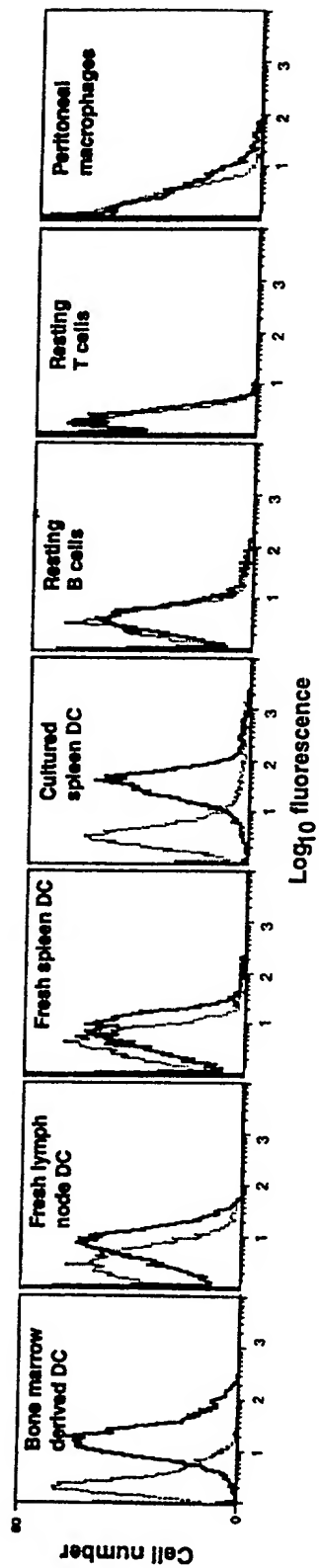


Figure 9

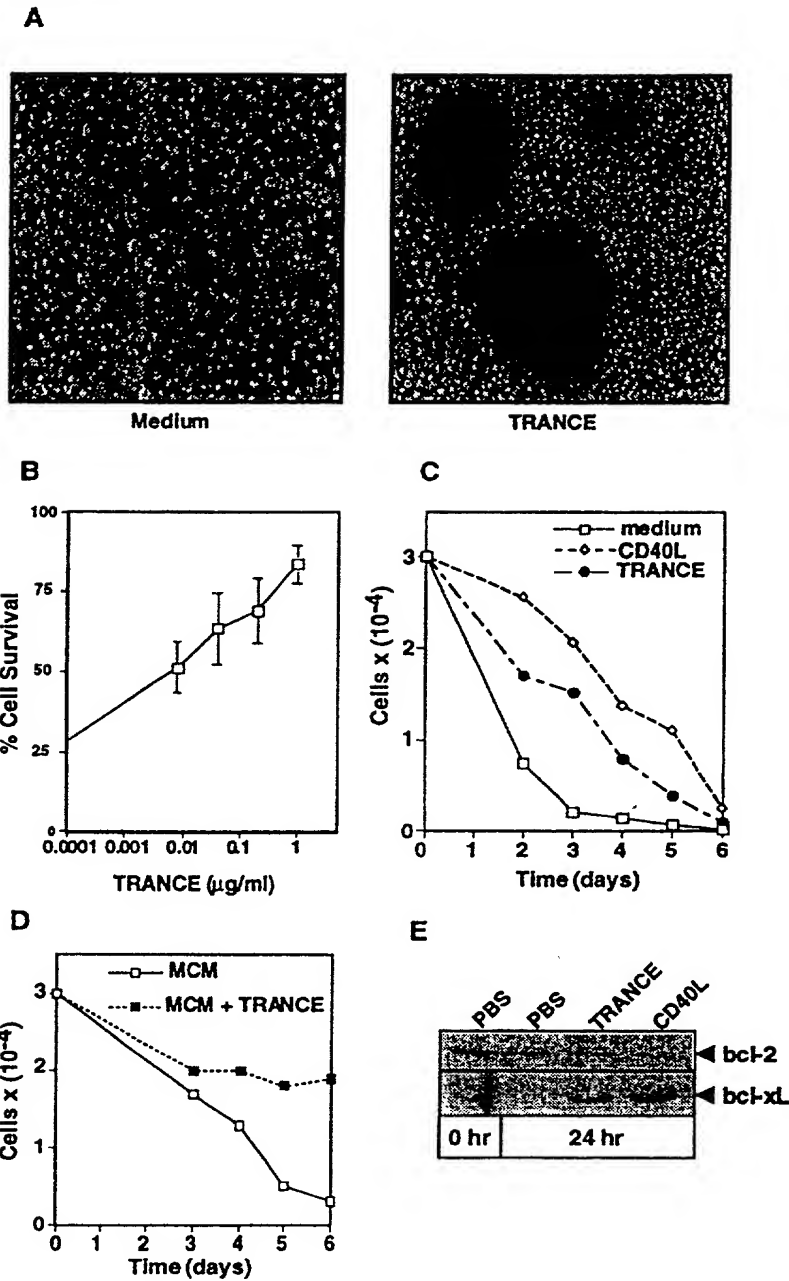


Figure 10

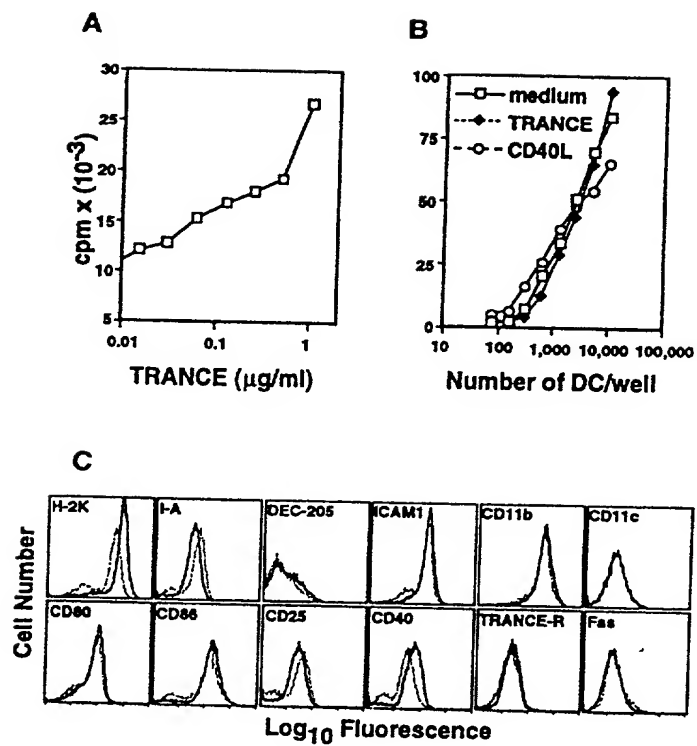


Figure 11

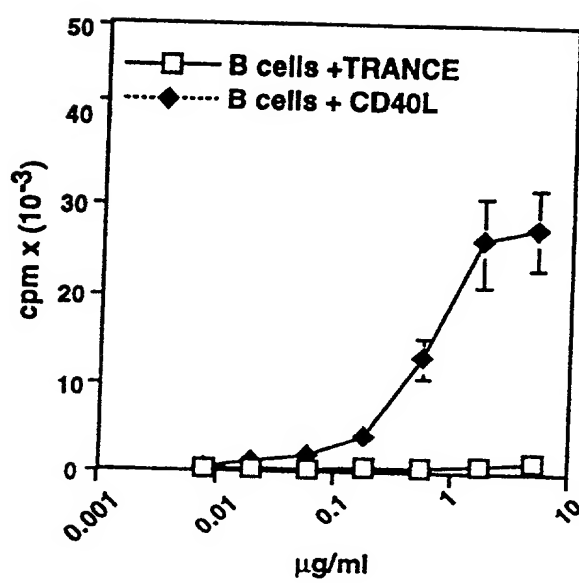


Figure 12

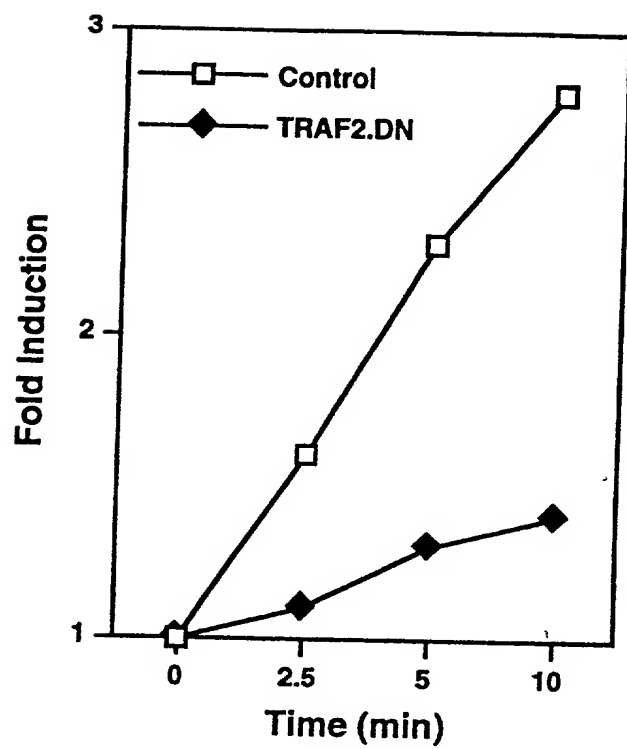


Figure 13